

**SEQUENCE LISTING**

<110> Brett P. Monia  
Jacqueline Wyatt

<120> ANTISENSE MODULATION OF INHIBITOR-KAPPA B KINASE-GAMMA EXPRESSION

<130> RTS-0191

<160> 88

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<212> DNA

<213> Homo sapiens

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gaggtcccat cagcccttgc cctgttgg atg aat agg cac ctc tgg aag agc Met Asn Arg His Leu Trp Lys Ser	1                   5	172
caa ctg tgt gag atg gtg cag ccc agt ggt ggc ccg gca gca gat cag Gln Leu Cys Glu Met Val Gln Pro Ser Gly Gly Pro Ala Ala Asp Gln	10               15                   20	220
gac gta ctg ggc gaa gag tct cct ctg ggg aag cca gcc atg ctg cac Asp Val Leu Gly Glu Ser Pro Leu Gly Lys Pro Ala Met Leu His	25               30                   35                   40	268
ctg cct tca gaa cag ggc gct cct gag acc ctc cag cgc tgc ctg gag Leu Pro Ser Glu Gln Gly Ala Pro Glu Thr Leu Gln Arg Cys Leu Glu	45               50                   55	316
gag aat caa gag ctc cga gat gcc atc cgg cag agc aac cag att ctg Glu Asn Gln Glu Leu Arg Asp Ala Ile Arg Gln Ser Asn Gln Ile Leu	60               65                   70	364
cgg gag cgc tgc gag gag ctt ctg cat ttc caa gcc agc cag agg gag Arg Glu Arg Cys Glu Glu Leu Leu His Phe Gln Ala Ser Gln Arg Glu	75               80                   85	412
gag aag gag ttc ctc atg tgc aag ttc cag gag gcc agg aaa ctg gtg Glu Lys Glu Phe Leu Met Cys Lys Phe Gln Glu Ala Arg Lys Leu Val	90               95                   100	460
gag aga ctc ggc ctg gag aag ctc gat ctg aag agg cag aag gag cag Glu Arg Leu Gly Leu Glu Lys Leu Asp Leu Lys Arg Gln Lys Glu Gln	105              110                   115                   120	508
gct ctg cgg gag gtg gag cac ctg aag aga tgc cag cag cag atg gct Ala Leu Arg Glu Val Glu His Leu Lys Arg Cys Gln Gln Gln Met Ala	125              130                   135	556
gag gac aag gcc tct gtg aaa gcc cag gtg acg tcc ttg ctc ggg gag Glu Asp Lys Ala Ser Val Lys Ala Gln Val Thr Ser Leu Leu Gly Glu	140              145                   150	604
ctg cag gag agc cag agt cgc ttg gag gct gcc act aag gaa tgc cag Leu Gln Glu Ser Gln Ser Arg Leu Glu Ala Ala Thr Lys Glu Cys Gln	155              160                   165	652
gct ctg gag ggt cgg gcc cgg gcc agc gag cag gcg cgg cag ctg Ala Leu Glu Gly Arg Ala Arg Ala Ser Glu Gln Ala Arg Gln Leu	170              175                   180	700
gag agt gag cgc gag gcg ctg cag cag cag cac agc gtg cag gtg gac Glu Ser Glu Arg Glu Ala Leu Gln Gln His Ser Val Gln Val Asp	185              190                   195                   200	748
cag ctg cgc atg cag ggc cag agc gtg gag gcc gcg ctc cgc atg gag Gln Leu Arg Met Gln Gly Gln Ser Val Glu Ala Ala Leu Arg Met Glu	205              210                   215	796
cgc cag gcc gcc tcg gag gag aag agg aag ctg gcc cag ttg cag gtg		844

Arg Gln Ala Ala Ser Glu Glu Lys Arg Lys Leu Ala Gln Leu Gln Val			
220	225	230	
gcc tat cac cag ctc ttc caa gaa tac gac aac cac atc aag agc agc			892
Ala Tyr His Gln Leu Phe Gln Glu Tyr Asp Asn His Ile Lys Ser Ser			
235	240	245	
gtg gtg ggc agt gag cg <sup>g</sup> aag cga gga atg cag ctg gaa gat ctc aaa			940
Val Val Gly Ser Glu Arg Lys Arg Gly Met Gln Leu Glu Asp Leu Lys			
250	255	260	
cag cag ctc cag cag gcc gag gag gcc ctg gtg gcc aaa cag gag gtg			988
Gln Gln Leu Gln Ala Glu Glu Ala Leu Val Ala Lys Gln Glu Val			
265	270	275	280
atc gat aag ctg aag gag gag gcc gag cag cac aag att gtg atg gag			1036
Ile Asp Lys Leu Lys Glu Glu Ala Glu Gln His Lys Ile Val Met Glu			
285	290	295	
acc gtt ccg gtg ctg aag gcc cag gc <sup>g</sup> gat atc tac aag gc <sup>g</sup> gac ttc			1084
Thr Val Pro Val Leu Lys Ala Gln Ala Asp Ile Tyr Lys Ala Asp Phe			
300	305	310	
cag gct gag agg cag gcc cg <sup>g</sup> gag aag ctg gcc gag aag aag gag ctc			1132
Gln Ala Glu Arg Gln Ala Arg Glu Lys Leu Ala Glu Lys Lys Glu Leu			
315	320	325	
ctg cag gag cag ctg gag cag ctg cag agg gag tac agc aaa ctg aag			1180
Leu Gln Glu Gln Leu Glu Gln Leu Gln Arg Glu Tyr Ser Lys Leu Lys			
330	335	340	
gcc agc tgt cag gag tcg gcc agg atc gag gac atg agg aag cg <sup>g</sup> cat			1228
Ala Ser Cys Gln Glu Ser Ala Arg Ile Glu Asp Met Arg Lys Arg His			
345	350	355	360
gtc gag gtc tcc cag gcc ccc ttg ccc ccc gcc cct gcc tac ctc tcc			1276
Val Glu Val Ser Gln Ala Pro Leu Pro Pro Ala Pro Ala Tyr Leu Ser			
365	370	375	
tct ccc ctg gcc ctg ccc agc cag agg agg agc ccc ccc gag gag cca			1324
Ser Pro Leu Ala Leu Pro Ser Gln Arg Arg Ser Pro Pro Glu Glu Pro			
380	385	390	
cct gac ttc tgc tgt ccc aag tgc cag tat cag gcc cct gat atg gac			1372
Pro Asp Phe Cys Cys Pro Lys Cys Gln Tyr Gln Ala Pro Asp Met Asp			
395	400	405	
acc ctg cag ata cat gtc atg gag tgc att gag tag ggccggccag			1418
Thr Leu Gln Ile His Val Met Glu Cys Ile Glu			
410	415		
tgcaaggcca ctgcctgccc gaggacgtgc ccgggaccgt gcagtctgcg ctttcctctc			1478
ccgcctgcct agcccaggat gaagggtctgg gtggccacaa ctggatgcc acctggagcc			1538
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accatgcaca cgggtgtct cctttggc tgcatgctat tccatggc agccagaccg	1898
atgtgtattt aaccagtcac tattgatgga catgggtt gtttccatc ttttggta	1958
cataaataat ggcatagtaa aaaaaaaaaaaa aaaaaaa	1994

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<223> PCR Primer

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<210> 8

<211> 20

<212> DNA

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gaagatggtg atgggatttc

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<210> 9

<211> 20

<212> DNA

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<223> PCR Probe

<400> 9

caagcttccc gttctcagcc

20

<210> 10

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<212> DNA

<213> Homo sapiens

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Met Asn

1

agg cac ctc tgg aag agc caa ctg tgt gag atg gtg cag ccc agt ggt  
Arg His Leu Trp Lys Ser Gln Leu Cys Glu Met Val Gln Pro Ser Gly

164

5

10

15

ggc ccg gca gca gat cag gac gta ctg ggc gaa gag tct cct ctg ggg Gly Pro Ala Ala Asp Gln Asp Val Leu Gly Glu Glu Ser Pro Leu Gly	20	25	30	212	
aag cca gcc atg ctg cac ctg cct tca gaa cag ggc gct cct gag acc Lys Pro Ala Met Leu His Leu Pro Ser Glu Gln Gly Ala Pro Glu Thr	35	40	45	50	260
ctc cag cgc tgc ctg gag gag aat caa gag ctc cga gat gcc atc cg Leu Gln Arg Cys Leu Glu Glu Asn Gln Glu Leu Arg Asp Ala Ile Arg	55	60	65		308
cag agc aac cag att ctg cgg gag cgc tgc gag gag ctt ctg cat ttc Gln Ser Asn Gln Ile Leu Arg Glu Arg Cys Glu Glu Leu Leu His Phe	70	75	80		356
caa gcc agc cag agg gag gag aag gag ttc ctc atg tgc aag ttc cag Gln Ala Ser Gln Arg Glu Glu Lys Glu Phe Leu Met Cys Lys Phe Gln	85	90	95		404
gag gcc agg aaa ctg gtg gag aga ctc ggc ctg gag aag ctc gat ctg Glu Ala Arg Lys Leu Val Glu Arg Leu Gly Leu Glu Lys Leu Asp Leu	100	105	110		452
aag agg cag aag gag cag gct ctg cgg gag gtg gag cac ctg aag aga Lys Arg Gln Lys Glu Gln Ala Leu Arg Glu Val Glu His Leu Lys Arg	115	120	125	130	500
tgc cag cag cag atg gct gag gac aag gcc tct gtg aaa gcc cag gtg Cys Gln Gln Gln Met Ala Glu Asp Lys Ala Ser Val Lys Ala Gln Val	135	140	145		548
acg tcc ttg ctc ggg gag ctg cag gag agc cag agt cgc ttg gag gct Thr Ser Leu Leu Gly Glu Leu Gln Glu Ser Gln Ser Arg Leu Glu Ala	150	155	160		596
gcc act aag gaa tgc cag gct ctg gag ggt cgg gcc cgg gcg gcc agc Ala Thr Lys Glu Cys Gln Ala Leu Glu Gly Arg Ala Arg Ala Ala Ser	165	170	175		644
gag cag gcg cgg cag ctg gag agt gag cgc gag gcg ctg cag cag cag Glu Gln Ala Arg Gln Leu Glu Ser Glu Arg Glu Ala Leu Gln Gln Gln	180	185	190		692
cac agc gtg cag gtg gac cag ctg cgc atg cag ggc cag agc gtg gag His Ser Val Gln Val Asp Gln Leu Arg Met Gln Gly Gln Ser Val Glu	195	200	205	210	740
gcc gcg ctc cgc atg gag cgc cag gcc gcc tcg gag gag aag agg aag Ala Ala Leu Arg Met Glu Arg Gln Ala Ala Ser Glu Glu Lys Arg Lys	215	220	225		788
ctg gcc cag ttg cag gtg gcc tat cac cag ctc ttc caa gaa tac gac Leu Ala Gln Leu Gln Val Ala Tyr His Gln Leu Phe Gln Glu Tyr Asp	230	235	240		836

aac cac atc aag agc agc gtg gtg ggc agt gag cg <sup>g</sup> aag cga gga atg Asn His Ile Lys Ser Ser Val Val Gly Ser Glu Arg Lys Arg Gly Met 245 250 255	884
cag ctg gaa gat ctc aaa cag cag ctc cag cag gcc gag gag gcc ctg Gln Leu Glu Asp Leu Lys Gln Gln Leu Gln Ala Glu Glu Ala Leu 260 265 270	932
gtg gcc aaa cag gag gtg atc gat aag ctg aag gag gag gcc gag cag Val Ala Lys Gln Glu Val Ile Asp Lys Leu Lys Glu Glu Ala Glu Gln 275 280 285 290	980
cac aag att gtg atg gag acc gtt ccg gtg ctg aag gcc cag gc <sup>g</sup> gat His Lys Ile Val Met Glu Thr Val Pro Val Leu Lys Ala Gln Ala Asp 295 300 305	1028
atc tac aag gc <sup>g</sup> gac ttc cag gct gag agg cag gcc cgg gag aag ctg Ile Tyr Lys Ala Asp Phe Gln Ala Glu Arg Gln Ala Arg Glu Lys Leu 310 315 320	1076
gcc gag aag aag gag ctc ctg cag gag cag ctg gag cag ctg cag agg Ala Glu Lys Lys Glu Leu Leu Gln Glu Gln Leu Glu Gln Leu Gln Arg 325 330 335	1124
gag tac aga aaa ctg aag gcc agc tgt cag gag tcg gcc agg atc gag Glu Tyr Arg Lys Leu Lys Ala Ser Cys Gln Glu Ser Ala Arg Ile Glu 340 345 350	1172
gac atg agg aag cgg cat gtc gag gtc tcc cag gcc ccc ttg ccc ccc Asp Met Arg Lys Arg His Val Glu Val Ser Gln Ala Pro Leu Pro Pro 355 360 365 370	1220
gcc cct gcc tac ctc tcc tct ccc ctg gcc ctg ccc agt cag agg agg Ala Pro Ala Tyr Leu Ser Ser Pro Leu Ala Leu Pro Ser Gln Arg Arg 375 380 385	1268
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cag gcc cct gat atg gac acc ctg cag ata cat gtc atg gag tgc att Gln Ala Pro Asp Met Asp Thr Leu Gln Ile His Val Met Glu Cys Ile 405 410 415	1364
gag tag ggccggccag tgcaaggcca ctgcctgccg aggacgtgcc cgggaccgtg Glu	1420
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ccatttgca gccagaccga tgtgtattta accagtcact attgatggac atttgggtg 1900  
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<210> 15

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<210> 24

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<400> 68  
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<400> 76  
cgcatctacc ccaaaaagagg 20

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<223> Antisense Oligonucleotide

<400> 83

gcaaaatgga atagcatgca

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agatggaaa caacccaaat 20

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<400> 86  
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<400> 87  
aaggctgtc agcagagtcc 20

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<400> 88  
tattcatcca acagggcaag 20